09/980881

JC10 Rec'd PCT/PTO 3 0 OCT 2001

SEQUENCE LISTING

<110> AKIRA MATSUMOTO

<120> Human Brain Carboxypeptidase B

<130> MAT-101PCT

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<150> JP 1999-125169

<151> 1999-04-30

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<170> PatentIn Ver. 2.0

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Ile Val Leu Phe Cys Glu Gln His Val Phe Ala Phe Gln Ser Gly Gln
15 20 25

gtt cta gct gct ctt cct aga acc tct agg caa gtt caa gtt cta cag 146
Val Leu Ala Ala Leu Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln
30 35 40

aat ctt act aca aca tat gag att gtt ctc tgg cag ccg gta aca gct 194
Asn Leu Thr Thr Thr Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala
45 50 55

gac ctt att gtg aag aaa aaa caa gtc cat ttt ttt gta aat gca tct 242
Asp Leu Ile Val Lys Lys Lys Gln Val His Phe Phe Val Asn Ala Ser
60 65 70 75

gat gtc gac aat gtg aaa gcc cat tta aat gtg agc gga att cca tgc 290
Asp Val Asp Asn Val Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys
80 85 90

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agt gtc ttg ctg gca gac gtg gaa gat ctt att caa cag cag att tcc    338
Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser
             95                 100                 105

aac gac aca gtc agc ccc cga gcc tcc gca tcg tac tat gaa cag tat    386
Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr
        110                 115                 120

cac tca cta aat gaa atc tat tct tgg ata gaa ttt ata act gag agg    434
His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg
    125                 130                 135

cat cct gat atg ctt aca aaa atc cac att gga tcc tca ttt gag aag    482
His Pro Asp Met Leu Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys
140                 145                 150                 155

tac cca ctc tat gtt tta aag gtt tct gga aaa gaa caa aca gcc aaa    530
Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys
                160                 165                 170

aat gcc ata tgg att gac tgt gga atc cat gcc aga gaa tgg atc tct    578
Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser
            175                 180                 185

cct gct ttc tgc ttg tgg ttc ata ggc cat aat cga atg tgg aga aag    626
Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys
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190 195 200

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Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn

205 210 215

agc aac ttt gtc tcc aaa cac tgg tgt gag gaa ggt gca tcc agt tcc 722

Ser Asn Phe Val Ser Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser

220 225 230 235

tca tgc tcg gaa acc tac tgt gga ctt tat cct gag tca gaa cca gaa 770

Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu

240 245 250

gtg aag gca gtg gct agt ttc ttg aga aga aat atc aac cag att aaa 818

Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys

255 260 265

gca tac atc agc atg cat tca tac tcc cag cat ata gtg ttt cca tat 866

Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr

270 275 280

tcc tat aca cga agt aaa agc aaa gac cat gag gaa ctg tct cta gta 914

Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val

285 290 295

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gcc agt gaa gca gtt cgt gct att gac aaa act agt aaa aat acc agg 962
Ala Ser Glu Ala Val Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg
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tat aca cat ggc cat ggc tca gaa acc tta tac cta gct cct gga ggt 1010
Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly
320 325 330

ggg gac gat tgg atc tat gat ttg ggc atc aaa tat tcg ttt aca tca 1058
Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser
335 340 345

aac cca cct gta gag aag ctt ttg ccg ctg tct cta aaa tagcttggca 1107
Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser Leu Lys
350 355 360

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<213> Homo sapiens

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Pro Arg Thr Ser Arg Gln Val Gln Val Leu Gln Asn Leu Thr Thr Thr

35 40 45

Tyr Glu Ile Val Leu Trp Gln Pro Val Thr Ala Asp Leu Ile Val Lys

50 55 60

Lys Lys Gln Val His Phe Phe Val Asn Ala Ser Asp Val Asp Asn Val

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65 70 75 80

Lys Ala His Leu Asn Val Ser Gly Ile Pro Cys Ser Val Leu Leu Ala

85 90 95

Asp Val Glu Asp Leu Ile Gln Gln Gln Ile Ser Asn Asp Thr Val Ser

100 105 110

Pro Arg Ala Ser Ala Ser Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu

115 120 125

Ile Tyr Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu

130 135 140

Thr Lys Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val

145 150 155 160

Leu Lys Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile

165 170 175

Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu

180 185 190

Trp Phe Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr

195 200 205

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Ala Asn Asn His Cys Ile Gly Thr Asp Leu Asn Ser Asn Phe Val Ser

210 215 220

Lys His Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr

225 230 235 240

Tyr Cys Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala

245 250 255

Ser Phe Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met

260 265 270

His Ser Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser

275 280 285

Lys Ser Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val

290 295 300

Arg Ala Ile Asp Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His

305 310 315 320

Gly Ser Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile

325 330 335

Tyr Asp Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu

340 345 350

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Lys Leu Leu Pro Leu Ser Leu Lys

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20 25 30

Gln Pro Val Thr Ala Asp Leu Ile Val Lys Lys Lys Gln Val His Phe

35 40 45

Phe Val Asn Ala Ser Asp Val Asp Asn Val Lys Ala His Leu Asn Val

50 55 60

Ser Gly Ile Pro Cys Ser Val Leu Leu Ala Asp Val Glu Asp Leu Ile

65 70 75 80

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Gln Gln Gln Ile Ser Asn Asp Thr Val Ser Pro Arg Ala Ser Ala Ser
85 90 95

Tyr Tyr Glu Gln Tyr His Ser Leu Asn Glu Ile Tyr Ser Trp Ile Glu
100 105 110

Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys Ile His Ile Gly
115 120 125

Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys Val Ser Gly Lys
130 135 140

Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys Gly Ile His Ala
145 150 155 160

Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe Ile Gly His Asn
165 170 175

Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn Asn His Cys Ile
180 185 190

Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His Trp Cys Glu Glu
195 200 205

Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys Gly Leu Tyr Pro
210 215 220

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Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe Leu Arg Arg Asn
225 230 235 240

Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser Tyr Ser Gln His
245 250 255

Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser Lys Asp His Glu
260 265 270

Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala Ile Glu Lys Thr
275 280 285

Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser Glu Thr Leu Tyr
290 295 300

Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp Leu Gly Ile Lys
305 310 315 320

Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu Leu Pro Leu Ser
325 330 335

Leu Lys

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<213> Homo sapiens

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Ser Trp Ile Glu Phe Ile Thr Glu Arg His Pro Asp Met Leu Thr Lys

20 25 30

Ile His Ile Gly Ser Ser Phe Glu Lys Tyr Pro Leu Tyr Val Leu Lys

35 40 45

Val Ser Gly Lys Glu Gln Thr Ala Lys Asn Ala Ile Trp Ile Asp Cys

50 55 60

Gly Ile His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Leu Trp Phe

65 70 75 80

Ile Gly His Asn Arg Met Trp Arg Lys Asn Arg Ser Phe Tyr Ala Asn

85 90 95

Asn His Cys Ile Gly Thr Asp Leu Asn Arg Asn Phe Ala Ser Lys His

100 105 110

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Trp Cys Glu Glu Gly Ala Ser Ser Ser Ser Cys Ser Glu Thr Tyr Cys

115 120 125

Gly Leu Tyr Pro Glu Ser Glu Pro Glu Val Lys Ala Val Ala Ser Phe

130 135 140

Leu Arg Arg Asn Ile Asn Gln Ile Lys Ala Tyr Ile Ser Met His Ser

145 150 155 160

Tyr Ser Gln His Ile Val Phe Pro Tyr Ser Tyr Thr Arg Ser Lys Ser

165 170 175

Lys Asp His Glu Glu Leu Ser Leu Val Ala Ser Glu Ala Val Arg Ala

180 185 190

Ile Glu Lys Thr Ser Lys Asn Thr Arg Tyr Thr His Gly His Gly Ser

195 200 205

Glu Thr Leu Tyr Leu Ala Pro Gly Gly Gly Asp Asp Trp Ile Tyr Asp

210 215 220

Leu Gly Ile Lys Tyr Ser Phe Thr Ser Asn Pro Pro Val Glu Lys Leu

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Leu Pro Leu Ser Leu Lys

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Asn Pro Thr Tyr Lys Phe Phe Glu
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ggttcatagg ccataatcga atgt 24

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synthesized primer sequence

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